

#8 5-9-2000

1631

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/458,366
 DATE: 05/09/2000
 TIME: 11:12:47

Input Set : A:\Sequence.txt
 Output Set: N:\CRF3\05092000\I458366.raw

4 <110> APPLICANT: Evans, Ronald M.
 5 Blumberg, Bruce
 7 <120> TITLE OF INVENTION: NOVEL STEROID-ACTIVATED NUCLEAR
 8 RECEPTORS AND USES THEREFOR
 10 <130> FILE REFERENCE: SALK2270-2
 12 <140> CURRENT APPLICATION NUMBER: 09/458,366
 13 <141> CURRENT FILING DATE: 1999-12-09
 15 <150> PRIOR APPLICATION NUMBER: 09/005,286
 16 <151> PRIOR FILING DATE: 1998-01-09
 18 <160> NUMBER OF SEQ ID NOS: 39
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 2068
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (583)...(1884)
 31 <223> OTHER INFORMATION: N is selected from A, C, T/U or G
 33 <400> SEQUENCE: 1
 34 ggcacgagga gatctaggtt caaattaatg ttgcccttag tggtaaagga cagagaccct 60
 35 cagactgatg aaatgcgctc agaattactt agacaaagcg gatatttgcc actctcttcc 120
 36 ccttttctctg tgtttttgta gtgaagagac ctgaaagaaa aaagtaggga gaacataatg 180
 37 agaacaaata cggtaaatctc ttcattttgct agttcaagtg ctggacttgg gacttaggag 240
 38 gggcaatgga gccgcttagt gcctacatct gacttggact gaaatatagg tgagagacaa 300
 39 gattgtctca tatccgggga aatcataacc tatgactagg acgggaagag gaagcactgc 360
 40 ctttacttca gtgggaatct cggcctcagc ctgcaagcca agtggtcaca gtgagaaaag 420
 41 caagagaata agctaatact cctgtcctga acaaggcagc ggctccttgg taaagctact 480
 42 ccttgatcga tcctttgcac cggattgttc aaagtggacc ccaggggaga agtcggagca 540
 43 aagaacttac caccaagcag tccaagaggc ccagaagcaa ac ctg gag gtg aga 594
 44 Leu Glu Val Arg
 45 1
 47 ccc aaa gaa agc tgg aac cat gct gac ttt gta cac tgt gag gac aca 642
 48 Pro Lys Glu Ser Trp Asn His Ala Asp Phe Val His Cys Glu Asp Thr
 49 5 10 15 20
 51 gag tct gtt cct gga aag ccc agt gtc aac gca gat gag gaa gtc gga 690
 52 Glu Ser Val Pro Gly Lys Pro Ser Val Asn Ala Asp Glu Glu Val Gly
 53 25 30 35
 55 ggt ccc caa atc tgc cgt gta tgt ggg gac aag gcc act ggc tat cac 738
 56 Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala Thr Gly Tyr His
 57 40 45 50
 59 ttc aat gtc atg aca tgt gaa gga tgc aag ggc ttt ttc agg agg gcc 786
 60 Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ala
 61 55 60 65
 63 atg aaa cgc aac gcc cgg ctg agg tgc ccc ttc cgg aag ggc gcc tgc 834
 64 Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg Lys Gly Ala Cys
 65 70 75 80

ENTERED

P5
1

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67 gag atc acc cgg aag acc cgg cga cag tgc cag gcc tgc cgc ctg cgc      882
68 Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala Cys Arg Leu Arg
69 85          90          95          100
71 aag tgc ctg gag agc ggc atg aag aag gag atg atc atg tcc gac gag      930
72 Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile Met Ser Asp Glu
73          105          110          115
75 gcc gtg gag gag agg cgg gcc ttg atc aag cgg aag aaa agt gaa cgg      978
76 Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys Lys Ser Glu Arg
77          120          125          130
79 aca ggg act cag cca ctg gga gtg cag ggg ctg aca gag gag cag cgg      1026
80 Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr Glu Glu Gln Arg
81          135          140          145
83 atg atg atc agg gag ctg atg gac gct cag atg aaa acc ttt gac act      1074
84 Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys Thr Phe Asp Thr
85          150          155          160
87 acc ttc tcc cat ttc aag aat ttc cgg ctg cca ggg gtg ctt agc agt      1122
88 Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly Val Leu Ser Ser
89 165          170          175          180
91 ggc tgc gag ttg cca gag cct ctg cag gcc cca tcg agg gaa gaa gct      1170
92 Gly Cys Glu Leu Pro Glu Pro Leu Gln Ala Pro Ser Arg Glu Glu Ala
93          185          190          195
95 gcc aag tgg agc cag gtc cgg aaa gat ctg tgc tct ttg aag gtc tct      1218
96 Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser Leu Lys Val Ser
97          200          205          210
W--> 99 ctg caa gct gcg ggg gga gga tgg cag tgt ctg gaa cta caa acn ccc      1266
W--> 100 Leu Gln Ala Ala Gly Gly Gly Trp Gln Cys Leu Glu Leu Gln Xaa Pro
101          215          220          225
103 agc cga cag tgg cgg aaa gag atc ttc tcc ctg ctg ccc cac atg gct      1314
104 Ser Arg Gln Trp Arg Lys Glu Ile Phe Ser Leu Leu Pro His Met Ala
105          230          235          240
107 gac atg tca acc tac atg ttc aaa ggc atc atc agc ttt gcc aaa gtc      1362
108 Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser Phe Ala Lys Val
109 245          250          255          260
111 atc tcc tac ttc agg gac ttg ccc atc gag gac cag atc tcc ctg ctg      1410
112 Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu
113          265          270          275
115 aag ggg gcc gct ttc gag ctg tgt caa ctg aga ttc aac aca gtg ttc      1458
116 Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe Asn Thr Val Phe
117          280          285          290
119 aac gcg gag act gga,acc tgg gag tgt ggc cgg ctg tcc tac tgc ttg      1506
120 Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu Ser Tyr Cys Leu
121          295          300          305
123 gaa gac act gca ggt ggc ttc cag caa ctt cta ctg gag ccc atg ctg      1554
124 Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Glu Pro Met Leu
125          310          315          320
127 aaa ttc cac tac atg ctg aag aag ctg cag ctg cat gag gag gag tat      1602
128 Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His Glu Glu Glu Tyr
129 325          330          335          340
131 gtg ctg atg cag gcc atc tcc ctc ttc tcc cca gac cgc cca ggt gtg      1650
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```

132 Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp Arg Pro Gly Val
133                               345                               350                               355
135 ctg cag cac cgc gtg gtg gac cag ctg cag gag caa ttc gcc att act      1698
136 Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln Phe Ala Ile Thr
137                               360                               365                               370
139 ctg aag tcc tac att gaa tgc aat cgg ccc cag cct gct cat agg ttc      1746
140 Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro Ala His Arg Phe
141                               375                               380                               385
143 ttg ttc ctg aag atc atg gct atg ctc acc gag ctc cgc agc atc aat      1794
144 Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu Arg Ser Ile Asn
145                               390                               395                               400
147 gct cag cac acc cag cgg ctg ctg cgc atc cag gac ata cac ccc ttt      1842
148 Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp Ile His Pro Phe
149 405                               410                               415                               420
151 gct acg ccc ctc atg cag gag ttg ttc ggc atc aca ggt agc      1884
152 Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr Gly Ser
153                               425                               430
155 tgagcggctg ccttgggtga caccttcgag aggcagccag acccagagcc ctctgagccg      1944
156 gcactcccgg gccaaagacag atggacactg ccaagagccg acaatgccct gctggcctgt      2004
157 ctccctaggg aattcctgct atgacagctg gctagcattc ctcaggaagg acatgggggtg      2064
158 cccc      2068
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 434
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Xaa is threonine
168 <400> SEQUENCE: 2
169 Leu Glu Val Arg Pro Lys Glu Ser Trp Asn His Ala Asp Phe Val His
170 1 5 10 15
171 Cys Glu Asp Thr Glu Ser Val Pro Gly Lys Pro Ser Val Asn Ala Asp
172 20 25 30
173 Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala
174 35 40 45
175 Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe
176 50 55 60
177 Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg
178 65 70 75 80
179 Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala
180 85 90 95
181 Cys Arg Leu Arg Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile
182 100 105 110
183 Met Ser Asp Glu Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys
184 115 120 125
185 Lys Ser Glu Arg Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr
186 130 135 140
187 Glu Glu Gln Arg Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys
188 145 150 155 160
189 Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly

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```

190                               165                               170                               175
191 Val Leu Ser Ser Gly Cys Glu Leu Pro Glu Pro Leu Gln Ala Pro Ser
192                               180                               185                               190
193 Arg Glu Glu Ala Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser
194                               195                               200                               205
195 Leu Lys Val Ser Leu Gln Ala Ala Gly Gly Gly Trp Gln Cys Leu Glu
196                               210                               215                               220
W--> 197 Leu Gln Xaa Pro Ser Arg Gln Trp Arg Lys Glu Ile Phe Ser Leu Leu
198 225                               230                               235                               240
199 Pro His Met Ala Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser
200                               245                               250                               255
201 Phe Ala Lys Val Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln
202                               260                               265                               270
203 Ile Ser Leu Leu Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe
204                               275                               280                               285
205 Asn Thr Val Phe Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu
206                               290                               295                               300
207 Ser Tyr Cys Leu Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu
208 305                               310                               315                               320
209 Glu Pro Met Leu Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His
210                               325                               330                               335
211 Glu Glu Glu Tyr Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp
212                               340                               345                               350
213 Arg Pro Gly Val Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln
214                               355                               360                               365
215 Phe Ala Ile Thr Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro
216                               370                               375                               380
217 Ala His Arg Phe Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu
218 385                               390                               395                               400
219 Arg Ser Ile Asn Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp
220                               405                               410                               415
221 Ile His Pro Phe Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr
222                               420                               425                               430
223 Gly Ser
226 <210> SEQ ID NO: 3
227 <211> LENGTH: 25
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: putative SXR response element from the steroid
233     hydroxylase, rCYP3A1
235 <400> SEQUENCE: 3
236 tagacagttc atgaagttca tctac
238 <210> SEQ ID NO: 4
239 <211> LENGTH: 25
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: putative SXR response element from the steroid
```

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Input Set : A:\Sequence.txt
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```

245      hydroxylase, rCYP3A2
247 <400> SEQUENCE: 4
248 taagcagttc ataaagttca tctac
250 <210> SEQ ID NO: 5
251 <211> LENGTH: 25
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: putative SXR response element from the steroid
257      hydroxylase, rUGT1A6
259 <400> SEQUENCE: 5
260 actgtagttc ataaagttca catgg
262 <210> SEQ ID NO: 6
263 <211> LENGTH: 26
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: putative SXR response element from the steroid
269      hydroxylase, rbCYP2C1
271 <400> SEQUENCE: 6
272 caatcagttc aacagggttc accaat
274 <210> SEQ ID NO: 7
275 <211> LENGTH: 33
276 <212> TYPE: DNA
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: putative SXR response element from the steroid
281      hydroxylase, rP450R
283 <400> SEQUENCE: 7
284 cacaggtgag ctgaggccag cagcaggtcg aaa
286 <210> SEQ ID NO: 8
287 <211> LENGTH: 27
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: putative SXR response element from the steroid
293      hydroxylase, rCYP2A1
295 <400> SEQUENCE: 8
296 gtgcaggttc aactggaggt caacatg
298 <210> SEQ ID NO: 9
299 <211> LENGTH: 27
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: putative SXR response element from the steroid
305      hydroxylase, rCYP2A2
307 <400> SEQUENCE: 9
308 gtgctggttc aactggaggt cagtatg
310 <210> SEQ ID NO: 10

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 05/09/2000

PATENT APPLICATION: US/09/458,366

TIME: 11:12:48

Input Set : A:\Sequence.txt

Output Set: N:\CRF3\05092000\I458366.raw

L:99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:197 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:197 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:197 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23